

GRF Errors Corrected by the STIC Systems Branch.

Serial Number: 08/700,737A

CRF Processing Date: 6/3/2003  
 Edited by: AT  
 Verified by: AT

**ENTERED**

**RECEIVED**  
 1600  
 6/3/2003  
 STIC Staff  
 CENTER 1600/2900

- ☒ Changed a file from non-ASCII to ASCII
- ☒ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.



1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/700,737A

DATE: 06/03/2003

TIME: 12:42:16

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\06032003\H700737A.raw

4 <110> APPLICANT: Ponath, Paul D.  
 5 Ringler, Douglas J.  
 6 Jones, S. Tarran  
 7 Newman, Walter  
 8 Saldanha, Jose  
 9 Bendig, Mary M.  
 11 <120> TITLE OF INVENTION: Humanized Immunoglobulin Reactive with  
 12 alpha4beta7 Integrin  
 14 <130> FILE REFERENCE: 1855.1017-000  
 16 <140> CURRENT APPLICATION NUMBER: 08/700,737A  
 17 <141> CURRENT FILING DATE: 1996-08-15  
 19 <160> NUMBER OF SEQ ID NOS: 67  
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 494  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Artificial Sequence  
 28 <220> FEATURE:  
 29 <223> OTHER INFORMATION: Mouse consensus sequence  
 W--> 31 <221> NAME/KEY: unsure  
 32 <222> LOCATION: (450)...(450)  
 33 <223> OTHER INFORMATION: n=A,T,G or C  
 W--> 35 <221> unsure  
 36 <222> LOCATION: (466)...(466)  
 37 <223> OTHER INFORMATION: n=A,T,G or C  
 W--> 39 <221> unsure  
 40 <222> LOCATION: (467)...(467)  
 41 <223> OTHER INFORMATION: n=A,T,G or C  
 W--> 43 <221> unsure  
 44 <222> LOCATION: (482)...(482)  
 45 <223> OTHER INFORMATION: n=A,T,G or C  
 W--> 47 <221> unsure  
 48 <222> LOCATION: (483)...(483)  
 49 <223> OTHER INFORMATION: n=A,T,G or C  
 W--> 51 <400> 1  
 52 ttackrgwmk wcatgrratg sasctrkrctc atyytcttct tggatatcaac agctacaagt 60  
 53 gtccactccc aggtccaact gcagcagcct ggggctgagc ttgtgaagcc tgggacttca 120  
 54 gtgaagctgt cctgcaaggg ttatggctac accttcacca gctactggat gcactgggtg 180  
 55 aagcagaggc ctggacaagg ccttgagtgg atcgagaga ttgatccttc tgagagtaat 240  
 56 actaactaca atcaaaaatt caagggcaag gccacattga ctgtagacat ttctccagc 300  
 57 acagcctaca tgcagctcag cagcctgaca tctgaggact ctgcggtcta ctattgtgca 360  
 58 agaggggggtt acgacggatg ggactatgct attgactact ggggtcaagg cacctcagtc 420  
 W--> 59 accgtctcct cagccaaaac gacaccrycn csyktmtmyc yysbdnnccc ykgrwscytg 480

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\06032003\H700737A.raw

```

60 gnnngaagctt      ggga                                494
62 <210> SEQ ID NO: 2
63 <211> LENGTH: 144
64 <212> TYPE: PRT
65 <213> ORGANISM: Artificial Sequence
67 <220> FEATURE:
68 <223> OTHER INFORMATION: Mouse consensus sequence
W--> 70 <221> NAME/KEY: UNSURE
71 <222> LOCATION: (2)...(6)
72 <223> OTHER INFORMATION: Xaa = Any Amino Acid
W--> 74 <221> UNSURE
75 <222> LOCATION: (8)...(8)
76 <223> OTHER INFORMATION: Xaa = Any Amino Acid
W--> 78 <400> 2
W--> 79 Met Xaa Xaa Xaa Xaa Xaa Ile Xaa Phe Leu Val Ser Thr Ala Thr Ser
80 1 5 10 15
81 Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
82 20 25 30
83 Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Gly Tyr Gly Tyr Thr Phe
84 35 40 45
85 Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
86 50 55 60
87 Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn
88 65 70 75 80
89 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Ile Ser Ser Ser
90 85 90 95
91 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
92 100 105 110
93 Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp
94 115 120 125
95 Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr
96 130 135 140
99 <210> SEQ ID NO: 3
100 <211> LENGTH: 428
101 <212> TYPE: DNA
102 <213> ORGANISM: Unknown
104 <220> FEATURE:
105 <223> OTHER INFORMATION: Mouse
W--> 107 <221> NAME/KEY: CDS
108 <222> LOCATION: (18)...(428)
W--> 110 <400> 3
111 ttacttgacg actcggg atg gga tgg agc tat atc atc ttc ttc ttg gta 50
112 Met Gly Trp Ser Tyr Ile Ile Phe Phe Leu Val
113 1 5 10
115 tca aca gct aca agt gtc cac tcc cag gtc caa ctg cag cag cct ggg 98
116 Ser Thr Ala Thr Ser Val His Ser Gln Val Gln Leu Gln Gln Pro Gly
117 15 20 25
119 gct gag ctt gtg aag cct ggg act tca gtg aag ctg tcc tgc aag ggt 146
120 Ala Glu Leu Val Lys Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Gly

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Input Set : A:\PTO.AMC.txt

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```

121          30          35          40
123 tat ggc tac acc ttc acc agc tac tgg atg cac tgg gtg aag cag agg 194
124 Tyr Gly Tyr Thr Phe Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg
125          45          50          55
127 cct gga caa ggc ctt gag tgg atc gga gag att gat cct tct gag agt 242
128 Pro Gly Gln Gly Leu Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser
129 60          65          70          75
131 aat act aac tac aat caa aaa ttc aag ggc aag gcc aca ttg act gta 290
132 Asn Thr Asn Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val
133          80          85          90
135 gac att tcc tcc agc aca gcc tac atg cag ctc agc agc ctg aca tct 338
136 Asp Ile Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser
137          95          100          105
139 gag gac tct gcg gtc tac tat tgt gca aga ggg ggt tac gac gga tgg 386
140 Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp
141          110          115          120
143 gac tat gct att gac tac tgg ggt caa ggc aca tca gtc acc 428
144 Asp Tyr Ala Ile Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
145          125          130          135

```

149 &lt;210&gt; SEQ ID NO: 4

150 &lt;211&gt; LENGTH: 137

151 &lt;212&gt; TYPE: PRT

152 &lt;213&gt; ORGANISM: Unknown

154 &lt;220&gt; FEATURE:

155 &lt;223&gt; OTHER INFORMATION: Mouse

157 &lt;400&gt; SEQUENCE: 4

```

158 Met Gly Trp Ser Tyr Ile Ile Phe Phe Leu Val Ser Thr Ala Thr Ser
159 1          5          10          15
160 Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
161          20          25          30
162 Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Gly Tyr Gly Tyr Thr Phe
163          35          40          45
164 Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
165          50          55          60
166 Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn
167 65          70          75          80
168 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Ile Ser Ser Ser
169          85          90          95
170 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
171          100          105          110
172 Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp
173          115          120          125
174 Tyr Trp Gly Gln Gly Thr Ser Val Thr
175          130          135

```

178 &lt;210&gt; SEQ ID NO: 5

179 &lt;211&gt; LENGTH: 535

180 &lt;212&gt; TYPE: DNA

181 &lt;213&gt; ORGANISM: Artificial Sequence

183 &lt;220&gt; FEATURE:

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Output Set: N:\CRF4\06032003\H700737A.raw

```

184 <223> OTHER INFORMATION: Mouse consensus sequence
W--> 186 <221> NAME/KEY: CDS
187 <222> LOCATION: (16)...(435)
W--> 189 <400> 5
190 cgattactag tcgac atg aag ttg cct gtt agg ctg ttg gtg ctt ctg ttg 51
191           Met Lys Leu Pro Val Arg Leu Leu Val Leu Leu Leu
192           1           5           10
194 ttc tgg att cct gtt tcc gga ggt gat gtt gtg gtg act caa act cca 99
195 Phe Trp Ile Pro Val Ser Gly Gly Asp Val Val Val Thr Gln Thr Pro
196           15           20           25
198 ctc tcc ctg cct gtc agc ttt gga gat caa gtt tct atc tct tgc agg 147
199 Leu Ser Leu Pro Val Ser Phe Gly Asp Gln Val Ser Ile Ser Cys Arg
200           30           35           40
202 tct agt cag agt ctt gca aag agt tat ggg aac acc tat ttg tct tgg 195
203 Ser Ser Gln Ser Leu Ala Lys Ser Tyr Gly Asn Thr Tyr Leu Ser Trp
204           45           50           55           60
206 tac ctg cac aag cct ggc cag tct cca cag ctc ctc atc tat ggg att 243
207 Tyr Leu His Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gly Ile
208           65           70           75
210 tcc aac aga ttt tct ggg gtg cca gac agg ttc agt ggc agt ggt tca 291
211 Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
212           80           85           90
214 ggg aca gat ttc aca ctc aag atc agc aca ata aag cct gag gac ttg 339
215 Gly Thr Asp Phe Thr Leu Lys Ile Ser Thr Ile Lys Pro Glu Asp Leu
216           95           100          105
218 gga atg tat tac tgc tta caa ggt aca cat cag ccg tac acg ttc gga 387
219 Gly Met Tyr Tyr Cys Leu Gln Gly Thr His Gln Pro Tyr Thr Phe Gly
220           110          115          120
222 ggg ggg acc aag ctg gaa ata aaa cgg gct gat gct gca cca act gta 435
223 Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val
224           125          130          135          140
226 tccatcttcc caccatccag taagcttggg aatccatatg actagtagat cctctagagt 495
227 cgacctgcag gcatgcaagc ttccctatag tgagtcgtat 535
229 <210> SEQ ID NO: 6
230 <211> LENGTH: 140
231 <212> TYPE: PRT
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Mouse consensus sequence
237 <400> SEQUENCE: 6
238 Met Lys Leu Pro Val Arg Leu Leu Val Leu Leu Leu Phe Trp Ile Pro
239 1           5           10           15
240 Val Ser Gly Gly Asp Val Val Val Thr Gln Thr Pro Leu Ser Leu Pro
241           20           25           30
242 Val Ser Phe Gly Asp Gln Val Ser Ile Ser Cys Arg Ser Ser Gln Ser
243           35           40           45
244 Leu Ala Lys Ser Tyr Gly Asn Thr Tyr Leu Ser Trp Tyr Leu His Lys
245           50           55           60
246 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gly Ile Ser Asn Arg Phe

```

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```

247 65          70          75          80
248 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
249          85          90          95
250 Thr Leu Lys Ile Ser Thr Ile Lys Pro Glu Asp Leu Gly Met Tyr Tyr
251          100          105          110
252 Cys Leu Gln Gly Thr His Gln Pro Tyr Thr Phe Gly Gly Gly Thr Lys
253          115          120          125
254 Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val
255          130          135          140
258 <210> SEQ ID NO: 7
259 <211> LENGTH: 112
260 <212> TYPE: PRT
261 <213> ORGANISM: Unknown
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Mouse
266 <400> SEQUENCE: 7
267 Asp Val Val Val Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Phe Gly
268 1          5          10          15
269 Asp Gln Val Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Ala Lys Ser
270          20          25          30
271 Tyr Gly Asn Thr Tyr Leu Ser Trp Tyr Leu His Lys Pro Gly Gln Ser
272          35          40          45
273 Pro Gln Leu Leu Ile Tyr Gly Ile Ser Asn Arg Phe Ser Gly Val Pro
274          50          55          60
275 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
276 65          70          75          80
277 Ser Thr Ile Lys Pro Glu Asp Leu Gly Met Tyr Tyr Cys Leu Gln Gly
278          85          90          95
279 Thr His Gln Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
280          100          105          110
283 <210> SEQ ID NO: 8
284 <211> LENGTH: 112
285 <212> TYPE: PRT
286 <213> ORGANISM: Homo sapiens
288 <400> SEQUENCE: 8
289 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
290 1          5          10          15
291 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
292          20          25          30
293 Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
294          35          40          45
295 Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
296          50          55          60
297 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
298 65          70          75          80
299 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
300          85          90          95
301 Leu Gln Thr Pro Gln Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
302          100          105          110

```

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 06/03/2003  
PATENT APPLICATION: US/08/700,737A      TIME: 12:42:17

Input Set : A:\PTO.AMC.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 450,466,467,482,483

Seq#:2; Xaa Pos. ~~2,3,4,5,6,8~~

Seq#:51; Xaa Pos. 33,100,103

Seq#:53; Xaa Pos. 106,107,110

Seq#:54; Xaa Pos. 115

Seq#:56; N Pos. 30